

SEQUENCE LISTING

<110> Butcher, Eugene C.
Campbell, James J.
Rottman, James B.
Wu, Lijan

<120> Modulation of Systemic Memory T Cell
Trafficking

<130> STAN-110CON

<140> Unassigned

<141> 2001-04-17

<150> 09/232,878

<151> 1999-01-15

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1677

<212> DNA

<213> H. sapiens

<220>

<221> CDS

<222> (183)...(1265)

<223> CCR4, Chemokine receptor coding sequence

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agaaaagcaa gctgcttctg gttgggcca gacctgcctt gaggagcctg tagagttaaa 180
aa atg aac ccc acg gat ata gca gat acc acc ctc gat gaa agc ata 227
Met Asn Pro Thr Asp Ile Ala Asp Thr Leu Asp Glu Ser Ile
1 5 10 15
tac agc aat tac tat ctg tat gaa agt atc ccc aag cct tgc acc aaa 275
Tyr Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys
20 25 30
gaa ggc atc aag gca ttt ggg gag ctc ttc ctg ccc cca ctg tat tcc 323
Glu Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser
35 40 45
ttg gtt ttt gta ttt ggt ctg ctt gga aat tct gtg gtg gtt ctg gtc 371
Leu Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val
50 55 60
ctg ttc aaa tac aag cgg ctc agg tcc atg act gat gtg tac ctg ctc 419
Leu Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu
65 70 75
aac ctt gcc atc tcg gat ctg ctc ttc gtg ttt tcc ctc cct ttt tgg 467

Asn Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp	80	85	90	95
ggc tac tat gca gca gac cag tgg gtt ttt ggg cta ggt ctg tgc aag	515			
Gly Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys		100	105	110
atg att tcc tgg atg tac ttg gtg ggc ttt tac agt ggc ata ttc ttt	563			
Met Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe		115	120	125
gtc atg ctc atg agc att gat aga tac ctg gcg ata gtg cac gcg gtg	611			
Val Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val		130	135	140
ttt tcc ttg agg gca agg acc ttg act tat ggg gtc atc acc agt ttg	659			
Phe Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu		145	150	155
gct aca tgg tca gtg gct gtg ttc gcc tcc ctt cct ggc ttt ctg ttc	707			
Ala Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe		160	165	170
agc act tgt tat act gag cgc aac cat acc tac tgc aaa acc aag tac	755			
Ser Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr		180	185	190
tct ctc aac tcc acg acg tgg aag gtt ctc agc tcc ctg gaa atc aac	803			
Ser Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn		195	200	205
att ctc gga ttg gtg atc ccc tta ggg atc atg ctg ttt tgc tac tcc	851			
Ile Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser		210	215	220
atg atc atc agg acc ttg cag cat tgt aaa aat gag aag aag aac aag	899			
Met Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys		225	230	235
gcg gtg aag atg atc ttt gcc gtg gtg gtc ctc ttc ctt ggg ttc tgg	947			
Ala Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp		240	245	250
aca cct tac aac ata gtg ctc ttc cta gag acc ctg gtg gag cta gaa	995			
Thr Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu		260	265	270
gtc ctt cag gac tgc acc ttt gaa aga tac ttg gac tat gcc atc cag	1043			
Val Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln		275	280	285
gcc aca gaa act ctg gct ttt gtt cac tgc tgc ctt aat ccc atc atc	1091			
Ala Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile		290	295	300
tac ttt ttt ctg ggg gag aaa ttt cgc aag tac atc cta cag ctc ttc	1139			
Tyr Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe		305	310	315

aaa acc tgc agg ggc ctt ttt gtg ctc tgc caa tac tgt ggg ctc ctc 1187
 Lys Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu 335
 320 325 330

caa att tac tct gct gac acc ccc agc tca tct tac acg cag tcc acc 1235
 Gln Ile Tyr Ser Ala Asp Thr Pro Ser Ser Ser Tyr Thr Gln Ser Thr 350
 340 345

atg gat cat gat ctt cat gat gct ctg tag gaaaaatgaa atgggtgaaat 1285
 Met Asp His Asp Leu His Asp Ala Leu *
 355 360

gcagagtcaa tgaacttttc cacattcaga gcttacttta aaattggtat ttttaggtaa 1345
 gagatccctg agccagtgtc aggaggaagg cttacaccca cagtggaaag acagcttctc 1405
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 <212> PRT
 <213> H. sapiens

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 Ser Asn Tyr Tyr Leu Tyr Glu Ser Ile Pro Lys Pro Cys Thr Lys Glu
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 Gly Ile Lys Ala Phe Gly Glu Leu Phe Leu Pro Pro Leu Tyr Ser Leu
 35 40 45
 Val Phe Val Phe Gly Leu Leu Gly Asn Ser Val Val Val Leu Val Leu
 50 55 60
 Phe Lys Tyr Lys Arg Leu Arg Ser Met Thr Asp Val Tyr Leu Leu Asn
 65 70 75 80
 Leu Ala Ile Ser Asp Leu Leu Phe Val Phe Ser Leu Pro Phe Trp Gly
 85 90 95
 Tyr Tyr Ala Ala Asp Gln Trp Val Phe Gly Leu Gly Leu Cys Lys Met
 100 105 110
 Ile Ser Trp Met Tyr Leu Val Gly Phe Tyr Ser Gly Ile Phe Phe Val
 115 120 125
 Met Leu Met Ser Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe
 130 135 140
 Ser Leu Arg Ala Arg Thr Leu Thr Tyr Gly Val Ile Thr Ser Leu Ala
 145 150 155 160
 Thr Trp Ser Val Ala Val Phe Ala Ser Leu Pro Gly Phe Leu Phe Ser
 165 170 175
 Thr Cys Tyr Thr Glu Arg Asn His Thr Tyr Cys Lys Thr Lys Tyr Ser
 180 185 190
 Leu Asn Ser Thr Thr Trp Lys Val Leu Ser Ser Leu Glu Ile Asn Ile
 195 200 205
 Leu Gly Leu Val Ile Pro Leu Gly Ile Met Leu Phe Cys Tyr Ser Met
 210 215 220
 Ile Ile Arg Thr Leu Gln His Cys Lys Asn Glu Lys Lys Asn Lys Ala
 225 230 235 240
 Val Lys Met Ile Phe Ala Val Val Val Leu Phe Leu Gly Phe Trp Thr

245 250 255
 Pro Tyr Asn Ile Val Leu Phe Leu Glu Thr Leu Val Glu Leu Glu Val
 260 265 270
 Leu Gln Asp Cys Thr Phe Glu Arg Tyr Leu Asp Tyr Ala Ile Gln Ala
 275 280 285
 Thr Glu Thr Leu Ala Phe Val His Cys Cys Leu Asn Pro Ile Ile Tyr
 290 295 300
 Phe Phe Leu Gly Glu Lys Phe Arg Lys Tyr Ile Leu Gln Leu Phe Lys
 305 310 315 320
 Thr Cys Arg Gly Leu Phe Val Leu Cys Gln Tyr Cys Gly Leu Leu Gln
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 Ile Tyr Ser Ala Asp Thr Pro Ser Ser Tyr Thr Gln Ser Thr Met
 340 345 350
 Asp His Asp Leu His Asp Ala Leu
 355 360

<210> 3
 <211> 538
 <212> DNA
 <213> H. sapiens

<220>
 <221> CDS
 <222> (53)...(337)
 <223> Coding sequence for TARC chemokine

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 Met Ala
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cca ctg aag atg ctg gcc ctg gtc acc ctc ctc ctg ggg gct tct ctg 106
 Pro Leu Lys Met Leu Ala Leu Val Thr Leu Leu Leu Gly Ala Ser Leu
 5 10 15

cag cac atc cac gca gct cga ggg acc aat gtg ggc cgg gag tgc tgc 154
 Gln His Ile His Ala Ala Arg Gly Thr Asn Val Gly Arg Glu Cys Cys
 20 25 30

ctg gag tac ttc aag gga gcc att ccc ctt aga aag ctg aag acg tgg 202
 Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys Thr Trp
 35 40 45 50

tac cag aca tct gag gac tgc tcc agg gat gcc atc gtt ttt gta act 250
 Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe Val Thr
 55 60 65

gtg cag ggc agg gcc atc tgt tgc gac ccc aac aac aag aga gtg aag 298
 Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg Val Lys
 70 75 80

aat gca gtt aaa tac ctg caa agc ctt gag agg tct tga agcctcctca 347
 Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser *
 85 90

cccagactc ctgactgtct cccgggacta cctgggacct ccaccgttgg tgttcaccgc 407
 cccacacctg agcgccctggg tccaggggag gccttccagg gacgaagaag agccacagtg 467
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tctttatcct c

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 <212> PRT
 <213> H. sapiens

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 20 25 30
 Cys Cys Leu Glu Tyr Phe Lys Gly Ala Ile Pro Leu Arg Lys Leu Lys
 35 40 45
 Thr Trp Tyr Gln Thr Ser Glu Asp Cys Ser Arg Asp Ala Ile Val Phe
 50 55 60
 Val Thr Val Gln Gly Arg Ala Ile Cys Ser Asp Pro Asn Asn Lys Arg
 65 70 75 80
 Val Lys Asn Ala Val Lys Tyr Leu Gln Ser Leu Glu Arg Ser
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<210> 5
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 <212> DNA
 <213> H. sapiens

<220>
 <221> CDS
 <222> (20)...(301)
 <223> Coding sequence for MDC chemokine

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 1 5 10
 ctc gtc ctc ctt gct gtg gcg ctt caa gca act gag gca ggc ccc tac 100
 Leu Val Leu Leu Ala Val Ala Leu Gln Ala Thr Glu Ala Gly Pro Tyr
 15 20 25
 ggc gcc aac atg gaa gac agc gtc tgc tgc cgt gat tac gtc cgt tac 148
 Gly Ala Asn Met Glu Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr
 30 35 40
 cgt ctg ccc ctg cgc gtg gtg aaa cac ttc tac tgg acc tca gac tcc 196
 Arg Leu Pro Leu Arg Val Val Lys His Phe Tyr Trp Thr Ser Asp Ser
 45 50 55
 tgc ccg agg cct ggc gtg gtg ttg cta acc ttc agg gat aag gag atc 244
 Cys Pro Arg Pro Gly Val Val Leu Leu Thr Phe Arg Asp Lys Glu Ile
 60 65 70 75
 tgt gcc gat ccc aga gtg ccc tgg gtg aag atg att ctc aat aag ctg 292
 Cys Ala Asp Pro Arg Val Pro Trp Val Lys Met Ile Leu Asn Lys Leu
 80 85 90
 agc caa tga agagcctact ctgatgaccg tggccttggc tcctccagga 341
 Ser Gln *

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aggctcagga gccctacctc cctgccatta tagctgctcc ccgccagaag cctgtgccaa 401
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<210> 6
 <211> 93
 <212> PRT
 <213> H. sapiens

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 20 25 30
 Asp Ser Val Cys Cys Arg Asp Tyr Val Arg Tyr Arg Leu Pro Leu Arg
 35 40 45

Val	Val	Lys	His	Phe	Tyr	Trp	Thr	Ser	Asp	Ser	Cys	Pro	Arg	Pro	Gly
	50					55					60				
Val	Val	Leu	Leu	Thr	Phe	Arg	Asp	Lys	Glu	Ile	Cys	Ala	Asp	Pro	Arg
65					70					75					80
Val	Pro	Trp	Val	Lys	Met	Ile	Leu	Asn	Lys	Leu	Ser	Gln			
				85					90						

TDZT40 = 9442E35D